

**Amendments to the Claims**

Please amend claims 1-4, 11, 12, 18-22, 25, and 26 as indicated in the listing of claims.

The listing of claims will replace all prior versions, and listings of claims in the application.

**Listing of Claims:**

1. (Currently Amended) A method for detecting the presence of a mammalian target neoplastic nucleic acid ~~having a mutant nucleotide sequence~~ in a neoplasm from a subject and the mammalian target neoplastic nucleic acid having presence of the same mutant nucleotide sequence nucleic acid in a tumor margin tissue specimen comprising:

extracting nucleic acid present in the neoplasm and in the tumor margin tissue specimen, wherein the tissue specimen is external to a primary neoplasm, and wherein the tissue specimen is histologically normal upon examination; and

detecting ~~the mutant~~ nucleotide sequences in the nucleic acid extracted from the neoplasm and in the nucleic acid extracted from the tissue specimen, wherein the target neoplastic nucleic acid to be detected is selected from the group consisting of APC, DCC, NF1, NF2, RET, VHL, and WT-1, ~~and wherein the mutant nucleotide sequence is present in the primary neoplasm and the tumor margin tissue.~~

2. (Currently Amended) The method of claim 1, further comprising, prior to detecting the ~~mutant~~ nucleotide sequences, amplifying the nucleic acid extracted from the tissue specimen to produce an amplified nucleic acid, wherein the detecting comprises detecting the presence of the ~~mutant~~ nucleotide sequence in the amplified nucleic acid.

3. (Currently Amended) The method of claim 2, wherein the amplifying is by means of oligonucleotides that hybridize to flanking regions of the ~~mutant~~ nucleotide sequence.

4. (Currently Amended) The method of claim 1, wherein the ~~mutant~~ nucleotide sequence contains a mutation selected from the group consisting of a restriction fragment length polymorphism, a nucleic acid deletion, and a nucleic acid substitution.

Claims 5-6 (Canceled).

7. (Previously presented) The method of claim 1, wherein the neoplasm is a neoplasm of the head or a neoplasm of the neck.

8. (Previously presented) The method of claim 1, wherein the neoplasm is head and neck cancer.

9. (Previously presented) The method of claim 1, wherein the neoplasm is a benign neoplasm.

10. (Previously presented) The method of claim 1, wherein the neoplasm is a malignant neoplasm.

11. (Currently Amended) The method of claim 2, further comprising, prior to detecting the ~~mutant~~ nucleotide sequence, cloning the amplified nucleic acid, wherein the detecting comprises detecting the presence of the ~~mutant~~ nucleotide sequence in the amplified nucleic acid.

12. (Currently Amended) A method for detecting metastases in a subject having an excised tumor, ~~the method~~ comprising:

a) isolating tissue from a surgical margin adjacent to the excised tumor, wherein the tissue is histologically normal upon examination;

b) contacting the tissue from the surgical margin with an oligonucleotide that specifically hybridizes to a mammalian target ~~neoplastic~~ nucleic acid having a ~~mutant nucleotide sequence~~ mutation, wherein the target ~~neoplastic~~ nucleic acid is selected from the group consisting of APC, DCC, NF1, NF2, RET, VHL, and WT-1, and wherein the ~~mutant nucleotide sequence~~ mutation is present in the primary neoplasm; and

c) detecting the ~~mutant nucleotide sequence~~ target nucleic acid, ~~when present in the tissue from the surgical margin~~, wherein the presence of the ~~mutant nucleotide sequence~~ target nucleic acid with the mutation in the tissue from the surgical margin is indicative of metastases.

13. (Canceled).

14. (Previously presented) The method according to claim 12 wherein the tissue is normal under a microscope.

Claims 15-17 (Canceled).

18. (Currently Amended) A method for detecting a mammalian target ~~neoplastic~~ nucleic acid having a ~~mutant nucleotide~~ mutation in the nucleic acid sequence in a tissue specimen which is external to a primary neoplasm, comprising isolating a tissue specimen wherein the tissue specimen is histologically normal, extracting nucleic acid present in the tissue specimen to obtain extracted nucleic acid, and detecting the presence of the ~~mutant nucleotide sequence~~ mutation in the extracted nucleic acid and in the tissue specimen, wherein the target ~~neoplastic~~ nucleic acid is selected from the group consisting of APC, DCC, NF1, NF2, RET, VHL, and WT-1, and wherein the ~~mutant nucleotide~~ mutation in the nucleic acid sequence is present in the primary neoplasm and in the tissue specimen.

19. (Currently Amended) A method for detecting a mammalian target ~~neoplastic~~ nucleic acid having a ~~mutant nucleotide~~ mutation in the nucleic acid sequence in a tumor margin tissue specimen which is external to a primary neoplasm, comprising isolating a tumor margin tissue specimen wherein the tissue specimen appears histologically normal, extracting nucleic acid present in the tissue specimen to obtain extracted nucleic acid, and detecting the presence of the ~~mutant nucleotide sequence~~ mutation in the extracted nucleic acid, wherein the target ~~neoplastic~~ nucleic acid is selected from the group consisting of APC, DCC, NF1, NF2, RET, VHL, and

WT-1, and wherein the ~~mutant nucleotide~~ mutation in the nucleic acid sequence is present in the primary neoplasm and in the tumor margin tissue.

20. (Currently Amended) A method for detecting the presence of a mammalian target ~~neoplastic~~ nucleic acid having a ~~mutant nucleotide~~ mutation in the nucleic acid sequence in a neoplasm and the mammalian target ~~neoplastic~~ nucleic acid having the same ~~mutant~~ nucleotide sequence in a lymph node tissue specimen, comprising:

isolating a lymph node tissue specimen wherein the tissue specimen is external to a primary neoplasm, and wherein the tissue specimen appears histologically normal;

extracting nucleic acid present in the neoplasm and in the tissue specimen and, wherein the target ~~neoplastic~~ nucleic acid is selected from the group consisting of APC, DCC, NF1, NF2, RET, VHL, and WT-1, and wherein the ~~mutant nucleotide~~ mutation in the nucleic acid sequence is present in the primary neoplasm;

and detecting the ~~mutant nucleotide sequence~~ mutation in the extracted nucleic acid from the neoplasm and in the extracted nucleic acid from the tissue specimen, when present in the tissue specimen.

21. (Currently Amended) The method of claim 20, further comprising, prior to detecting the ~~mutant nucleotide~~ nucleic acid sequence, amplifying the extracted nucleic acid from the tissue specimen to produce an amplified nucleic acid, wherein the detecting comprises detecting the presence of the ~~mutant~~ nucleotide sequence in the amplified nucleic acid.

22. (Currently Amended) The method of claim 20, wherein the ~~mutant nucleotide~~ nucleic acid sequence contains a mutation selected from the group consisting of a restriction fragment length polymorphism, a nucleic acid deletion, and a nucleic acid substitution.

23. (Canceled).

24. (Previously presented) The method of claim 20, wherein the neoplasm is a neoplasm of the head or a neoplasm of the neck.

25. (Currently Amended) A method for detecting metastases in a subject having an excised tumor, ~~the method~~ comprising:

a) isolating tissue from a lymph node, which is external to a primary neoplasm, and wherein the tissue appears histologically normal;

b) contacting the tissue with an oligonucleotide that specifically hybridizes to a mammalian target ~~neoplastic~~ nucleic acid having a ~~mutant nucleotide sequence~~ mutation, wherein the target ~~neoplastic~~ nucleic acid is selected from the group consisting of APC, DCC, NF1, NF2, RET, VHL, and WT-1, and wherein the ~~mutant nucleotide sequence~~ mutation is present in the primary neoplasm; and

c) detecting the presence of the ~~mutant nucleotide sequence~~ mutation in the tissue from the lymph node, wherein the presence of the ~~mutant nucleotide sequence~~ mutation in the tissue from the lymph node indicates metastases.

26. (Currently Amended) The method of claim 25, wherein no more than an average of about one out of every ten thousand cells of the tissue have a ~~mutant nucleotide~~ mutation in the nucleic acid sequence.

Claims 27-31 (Canceled).